

Fig.1

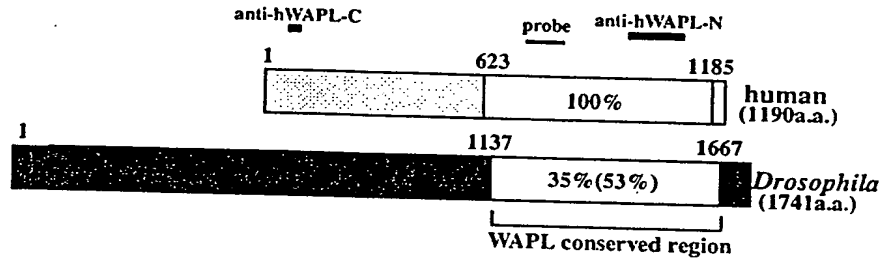


Fig. 2

hWAPL: 623 LKCRREDKELYTVVQHVKHFNDDVEFGENQEFTDDIEYLLSGLKSTQPLNTRCLSVISLA 682
 ++ R+ K+ Y VV++VK ++ E GE QE DD+EY+L L+ P TRCLS + LA
 dWAPL: 1137 IRVDRKTKDYYPVVRNVKTAHQIQEIGEYQEMDDDDVEYILDALQPHNPPATRCLSALQLA 1196

hWAPL: 683 TKCAMPSFRMHLRAHGMVAMVFKTLDDSQHHQNLSLCTAALMYILSRDRNLNMDLDRASLD 742
 KC MP+FRMH+RAHG+V FK L D+ +L LCT+A+MYILS++ LNMDLDR SL+
 dWAPL: 1197 AKCMMPAFRMHVRAHGVVTKFFKALSDANKDLSLGLCTSAIMYILSQEGLNMDLDRDSLE 1256

hWAPL: 743 LMIRLLELEQDASSAKL--LNEKDMNKIKEKIRRLCETV----HNKHLDLNITTGHLAM 796
 LMI LLE + S + + ++ K+K+R LCE + HL++++T G LAM
 dWAPL: 1257 LMINLLEADGVGGSTETGHS DRAGYDRNKQKVRELCEEIKAQKGKTHLNVDLSLTVGTLM 1316

hWAPL: 797 ETLLSLTSKRAGDWFKEELRLLGGLDHIVDKVKE-CVDHLSRDED---EKLVLASLWGAE 852
 ETLLSLTSKRAG+WFKE+LR LGGL+HI+ + + C ++ D + + L+ ++
 dWAPL: 1317 ETLLSLTSKRAGEWFKEDLRKLGGLEHIKTIISDFCRPVIACDTEIDWQPTLLDNMQTV 1376

hWAPL: 853 RCLRVLESVTVHNPENQSYLIAKDSQLIVSSAKALQHCEELIQQYNRAEDSICLADSKP 912
 RCLRVLE+VT HN NQ Y++ + + E L Q Y I L S
 dWAPL: 1377 RCLRVLENTQHNETNQRYMLTSGQGKAV-----ETLCQLYRLCSRQIMLHPSD- 1425

hWAPL: 913 LPHQNVTNHVGKAVEDCMRAIIGVLLNLTND-NE----WGSTKTGEQDGLIGTALNCVLQ 967
 + H G A+ + + ++ VL+NLT+ NE G+ G++ ++ T+ +L
 dWAPL: 1426 -GGGSNKEHPGVAMRELLVPVLKVLINLTHTFNEAQP SLGAELLGQRGDVVETSFRLLLL 1484

hWAPL: 968 VPKYLPQEQRFDIRVLGLGLLINLVEYSARNRHCLVNMETSCSFDSSICSGEGDSDLRIG 1027
 Y+P + F++ +L L LLINL ++ NR L+ + + D+
 dWAPL: 1485 SANYIPDQC VFELSILVLTLLINLCMHTVPNRAALMQAAAPAEYVA-----DNPPAQ 1536

hWAPL: 1028 GQVHAVQALVQLFLERERAAQLAESKTDELIKDAPTTQHDKSGEWQETSGEIQWVSTEKT 1087
 G V A+QAL++ F + E A+L E TD ++ ++K + QE E
 dWAPL: 1537 GSVSALQALLEYFYKCEELARLVEKNTDAFLE-----SNEKGKKKQEEVEE----- 1582

hWAPL: 1088 DGTEEKHKKEEEDLDLNLKALQHAGKHMEDCIVASYTALLGCLCQESPINVTTVREYL 1147
 +N +Q AG HME + SY A+L+G L ++ + + VR L
 dWAPL: 1583 -----TVNNLVQRAGHHMEHTLKGSYAAILVGNLIADNELYESVVRRL 1626

hWAPL: 1148 PEGDFSIMTEMLKKFLSFMNLT---AVGTTGQKSISRVE 1185
 F + +L+K+ +FMNLT A KS R+I+
 dWAPL: 1627 RGNSFKEIIGVLEKYHTFMNLTSSLEAAFAHMKSTKRIID 1667

>pir:T13610 [T13610] parallel sister chromatids protein - fruit fly
 Length = 1741

Identities = 204/581 (35%), Positives = 309/581 (53%), Gaps = 68/581 (11%)

Fig.3

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1  MTSRFCKTYSRKGCGSSKFOEVFSHKRTTLLSTWGETTFMAKLCQKRPNFKPDICEIPK
1  MTSRFCKTYSRKGCGSSKFOEVFSHKRTTLLSTWGETTFMAKLCQKRPNFKPDICEIPK

61  KPKVEESITGDPFGFSDDESIPVSSNLAQVCSYSSESSEAAQLEEVTSVLEANSKPS
61  KPKVEEEDTGPFGFSDDESIPVSSKILAQVCSYSSESSEAAQLEEVTSVLEANSKPS

121  HVVVEETVYSEKQYEDTLCKEKSRIKIVEDASISSCKLITSDKVENFEEHEKNS
121  HVVVEETVYSEKQYEDTLCKEKSRIKIVEDASISSCKLITSDKVENFEEHEKNS

181  HHQKNAEDSTKKNPAETVASEITETN-----DTWNSQFKKRESFSEISHKGSVRTC
181  HHQKNAEDSTKKNPAETVASEITETN-----DTWNSQFKKRESFSEISHKGSVRTC

237  LIEWNDNFEDIRSEDCLSLGDDFLLEMKDDDKN---RLLENLNEALFEEDVOSVLRKPS
241  LIEWNDNFEDIRSEDCLSLGDDFLLEMKDDDKN---RLLENLNEALFEEDVOSVLRKPS

294  CRTYCRANFTLSSGASNFDKLMDGTSCSLAKANSESSKDGLENQAKKQVSCGTSFRCTV
301  CRTYCRANFTLSSGASNFDKLMDGTSCSLAKANSESSKDGLENQAKKQVSCGTSFRCTV

354  GATRDYTVLHPSCLSVCNVTIQDTMERSMDEFTASTPADLGEAGRLKKADIATSKTTR
361  GATRDYTVLHPSCLSVCNVTIQDTMERSMDEFTASTPADLGEAGRLKKADIATSKTTR

414  FRPSNTRSKMDVKLEFFGFEDHETGCGGSGSSNYKIKYFCFDLSESEDDDDDCQV
421  FRPSNTRSKMDVKLEFFGFEDHETGCGGSGSSNYKIKYFCFDLSESEDDDDDCQV

473  ERRTSKKRTKTAPSPSPPPESDNSQDSQSCANNAENLDFTEDLPGVPESVKKPIKSK
481  ERRTSKKRTKTAPSPSPPPESDNSQDSQSCANNAENLDFTEDLPGVPESVKKPIKSK

533  GDKSKENTRKIESGPKRSPTKAVYNARHWNHPDSEELPGPPIKPORVTVRLSSKEPNQK
541  GDKSKENTRKIESGPKRSPTKAVYNARHWNHPDSEELPGPPIKPORVTVRLSSKEPNQK

593  DDGVFKAPAPSKVIKTVTIPTQFYCLIVTALKCFEDKELYTVVQHVKKHNDVVEFGEN
601  DDGVFKAPAPSKVIKTVTIPTQFYCLIVTALKCFEDKELYTVVQHVKKHNDVVEFGEN

653  QEFTHDIEYLLSGLKSTQPLNTRCLSVISLATKCAMPSFRMHILRAHGMVAMVFKTLDDSC
661  QEFTHDIEYLLSGLKSTQPLNTRCLSVISLATKCAMPSFRMHILRAHGMVAMVFKTLDDSC

713  HHQNLSLCTAALMYILSRDLNMDLDRASLDLMIRIVLEQDASSAKLLNEKDMIKIKER
721  HHQNLSLCTAALMYILSRDLNMDLDRASLDLMIRIVLEQDASSAKLLNEKDMIKIKER

773  IRRLCETVHKKHLDLENITGHLAMETLLSLTSKRAGDNFKEELRLGGLDHIIVDKVREC
781  IRRLCETVHKKHLDLENITGHLAMETLLSLTSKRAGDNFKEELRLGGLDHIIVDKVREC

833  VDHLSRLDEDEKLVASLWGAERCLRVLESVTVHNPENQSYLIAYKDSQLIVSSAKALQH
841  VDHLSRLDEDEKLVASLWGAERCLRVLESVTVHNPENQSYLIAYKDSQLIVSSAKALQH

892  CEELICQYHRAFSIQVADSPLRCHVTNHVGHAVEDCMRAIIGVLLNLNDNEWGSTR
901  CEELICQYHRAFSIQVADSPLRCHVTNHVGHAVEDCMRAIIGVLLNLNDNEWGSTR

952  TGEELGLIGTANCVLQVPKYLPCQRFDIRVLGLGLLINLVEYSARNRHCLVNNMTSCS
961  TGEELGLIGTANCVLQVPKYLPCQRFDIRVLGLGLLINLVEYSARNRHCLVNNMTSCS

1012  FDSSTCSGEGD-SLRIGQVHAVQALVQLFLERERAAQLAESKTDIELKDAPTTHQDKSG
1021  FDSSTCSGEGD-SLRIGQVHAVQALVQLFLERERAAQLAESKTDIELKDAPTTHQDKSG

1072  EWQETSCEIQWVSTKTDCEERKKEEEDDELDLNKALQHAGKHMEDCIVASYTALLC
1081  EWQETSCEIQWVSTKTDCEERKKEEEDDELDLNKALQHAGKHMEDCIVASYTALLC

1132  CLCQESPINVTIVREYLFEGDFSIMTEMLKKFLSFMILTCAVGTGQKSISRVIYELHC
1141  CLCQESPINVTIVREYLFEGDFSIMTEMLKKFLSFMILTCAVGTGQKSISRVIYELHC
    
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The upper and the lower rows are the sequences of the human and the mouse WAPLs, respectively. White and gray parts indicate the same and similar amino acids, respectively. The part in the frame is a region having similarity to the *Drosophila* WAPL.

Fig.4

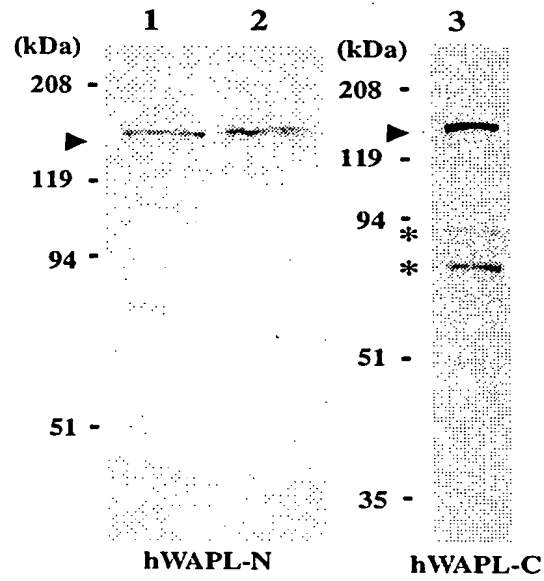


Fig.5

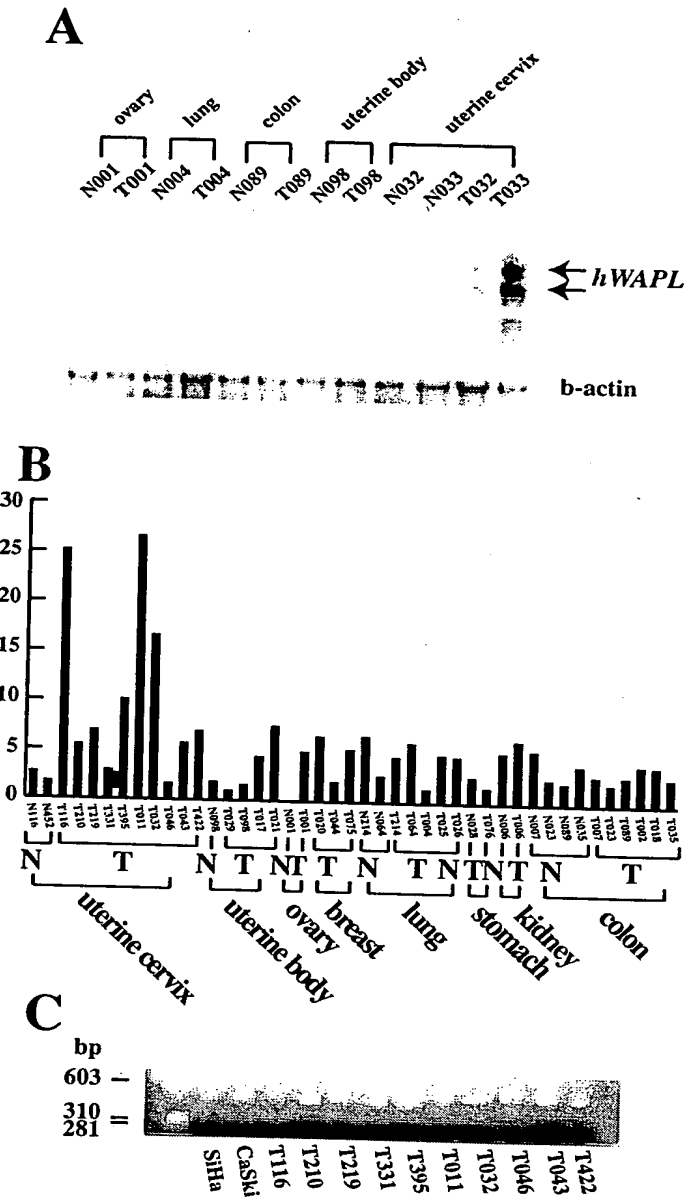
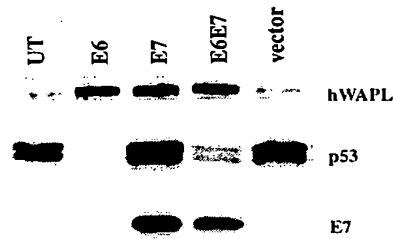


Fig. 6

A



B

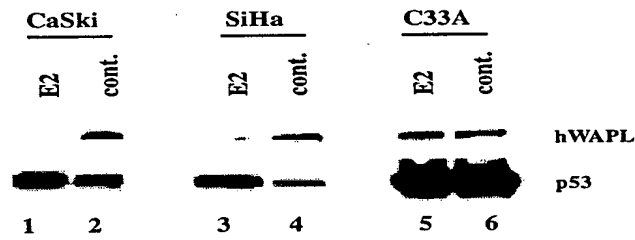
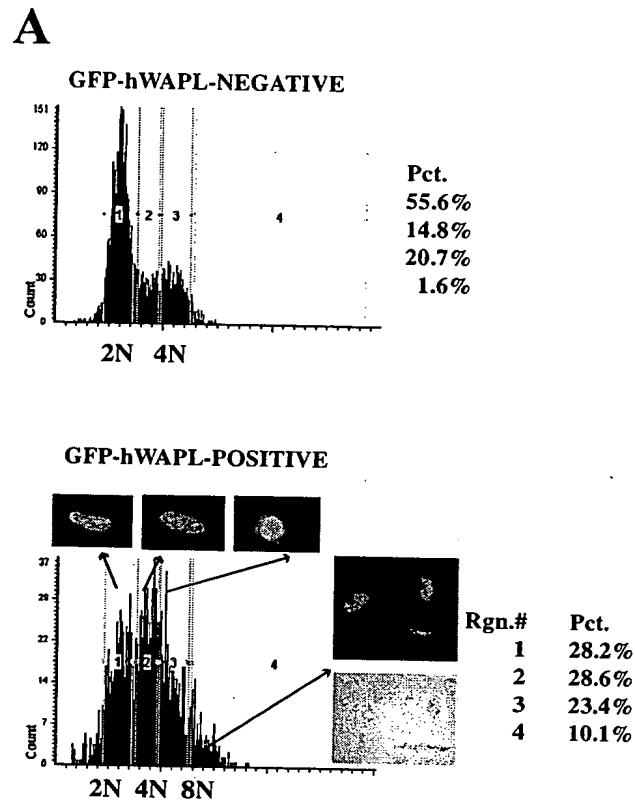


Fig. 7



B

micronuclei	+	-	total
GFP-hWAPL-NEGATIVE	60	940	1000
GFP-hWAPL-POSITIVE	124	876	1000

$p < 0.01$

Fig. 8

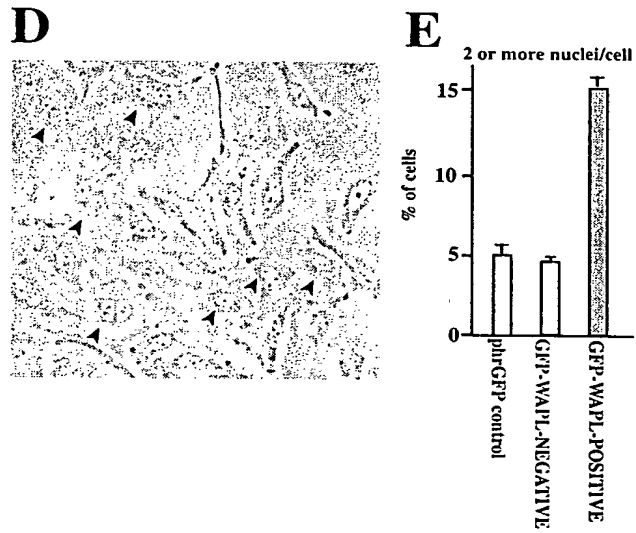
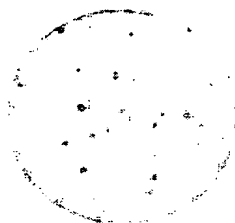


Fig.9

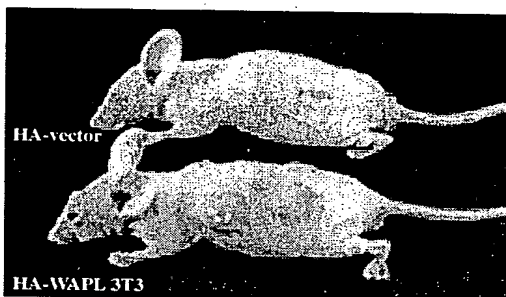
A

HA-WAPL 3T3

HA-3T3



B



C

1 2 3 4 5 6



anti-hWAPL-C



HA

D

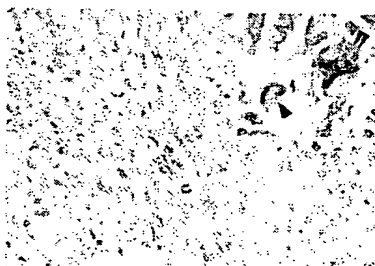


Fig.10

